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Db        241 SAKAVLTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300

Qy        301 VQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAAS 360

Qy        361 KNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTR 420

Qy        421 IKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHV 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHV 480

Qy        481 ASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQG 540

Qy        541 FTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQ 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQ 600

Qy        601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVN 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVN 660

Qy        661 VADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGD 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGD 720

Qy        721 AALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780

Qy        781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLA 840

Qy        841 HGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALS 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 HGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALS 900

Qy        901 SGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 SGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLG 960

Qy        961 LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTL 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTL 1020

Qy       1021 NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLW 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 NTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLW 1080

Qy       1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140

Qy       1141 KSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 KSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVT 1200

Qy       1201 GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
              ||||||||||||||||||||||||||||||||||||||||
Db       1201 GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
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RESULT 2
US-10-199-937-107
Sequence 107, Application US/10199937
Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik


```
;  APPLICANT:  DeMaggio, Anthony J.
;  APPLICANT:  Goldman, Phyllis S.
;  APPLICANT:  McElligott, David L.
;  TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
;  FILE REFERENCE: 27866/36559
;  CURRENT APPLICATION NUMBER: US/10/199,937
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US/09/606,035
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/141,582
;  PRIOR FILING DATE: 1999-06-29
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 1262
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-199-937-107

  Query Match             98.6%;  Score 6375.5;  DB 4;  Length 1262;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 1225;  Conservative    1;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          6 RGAAGGQGAQRGARVGAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLAL 65
              ||: |     |||| |  |||||||||||||||||||||||||||||||||||||||||||
Db         29 RGSRGAGSPARGAR-GRGHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLAL 87

Qy         66 LLAVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 LLAVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNS 147

Qy        126 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL 207

Qy        186 RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV 267

Qy        246 LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 327

Qy        306 QHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVE 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 QHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVE 387

Qy        366 VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL 447

Qy        426 SLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 SLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA 507

Qy        486 HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQ 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQ 567

Qy        546 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 627

Qy        606 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLW 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLW 687

Qy        666 KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD 725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD 747

Qy        726 AAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        748 AAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807

Qy        786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADP 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADP 867

Qy        846 TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS 927

Qy        906 PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM 987

Qy        966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS 1047

Qy       1026 GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH 1107

Qy       1086 RRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQY 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 RRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQY 1167

Qy       1146 VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1227

Qy       1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
              ||||||||||||||||||||||||||||||||||
Db       1228 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1262
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RESULT 3
US-10-199-937-133
; Sequence 133, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christensen, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-133

Query Match 98.6%; Score 6375.5; DB 4; Length 1385;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

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Qy          6 RGAAGGQGAQRGARVGAAHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLAL 65
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Db        152 RGSRGAGSPARGAR-GRGHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLLRLLAL 210

Qy         66 LLAVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 LLAVAAARIMSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNS 270

Qy        126 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLL 330

Qy        186 RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV 245
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 RHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAV 390

Qy        246 LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 LTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 450

Qy        306 QHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVE 365
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 QHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVE 510

Qy        366 VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL 425
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 VCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHL 570

Qy        426 SLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA 485
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 SLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKA 630

Qy        486 HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQ 545
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 HNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQ 690

Qy        546 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 605
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 MGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 750

Qy        606 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLW 665
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLW 810

Qy        666 KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD 725
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 KFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLD 870

Qy        726 AAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 AAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930

Qy        786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADP 845
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADP 990

Qy        846 TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS 905
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 TLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSS 1050

Qy        906 PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM 965
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 PSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLM 1110

Qy        966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS 1025
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1111 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGS 1170

Qy       1026 GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH 1085
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTH 1230

Qy       1086 RRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQY 1145
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 RRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQY 1290

Qy       1146 VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1205
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 VYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1350

Qy       1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG 1240
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Db        727 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 786

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 846

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 906

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1026

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1086

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
                ||||||||||||||||||||||||||||||||||||||||||||
Db       1087 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1131
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RESULT 6
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135

Query Match 99.9%; Score 5582; DB 4; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60
              |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 126

Qy         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 186

Qy        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 246

Qy        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 306

Qy        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 366

Qy        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 426

Qy        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 486

Qy        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546

Qy        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 606

Qy        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 666

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 786

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 846

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 906

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1026

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1086

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1087 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1131
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RESULT 7
US-10-199-937-2
; Sequence 2, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582

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Db        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDPSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Db        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Db        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Db        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYLAENSSKSNQYVYGIGGGTGCPVHKD 1020

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065

Db       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
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RESULT 13
US-09-509-196A-2
; Sequence 2, Application US/09509196A
; Patent No. US20020037582A1
; GENERAL INFORMATION:
; APPLICANT: DALY, Roger J.
; APPLICANT: SUTHERLAND, Robert L.
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 1871-129
; CURRENT APPLICATION NUMBER: US/09/509,196A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: P09388
; PRIOR FILING DATE: 1997-09-23
; PRIOR APPLICATION NUMBER: PCT AU98/00795
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-196A-2

Query Match 97.1%; Score 5421; DB 3; Length 1074;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1034; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy          27 IPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTI 86

Db           1 IPLHNACSFGHAEVVNLLLRHGADPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTI 60

Qy          87 RNTDGRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKS 146

Db          61 RNTDGRTALDLADPSAKAVLTGEYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKS 120

Qy         147 TPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNA 206

Db         121 TPLHLAAGYNRVKIVQLLLQHGRDVHAKDKGDLVPLHNACSYGHYEVTELLVKHGGCVNA 180

Qy         207 MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKG 266

Db         181 MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCKNKSAIDLAPTPQLKERLAYEFKG 240

Qy         267 HSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGAN 326

Db         241 HSLLQAAREADVTRIKKHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGAN 300

Qy         327 INEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLL 386

Db         301 INEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLL 360

Qy         387 LSYGCDPNIISLQGFTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLC 446

Db         361 LSYGCDPNIISLQGFTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLC 420

Qy         447 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHY 506

Db         421 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHY 480

Qy         507 EVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV 566

Db         481 EVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLV 540

Qy         567 KDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL 626

Db         541 KDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNL 600

Qy         627 EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEA 686

Db         601 EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNASLNATDKWAFTPLHEA 660

Qy         687 AQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVL 746

Db         661 AQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQVL 720

Qy         747 NGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVP 806

Db         721 NGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEVP 780

Qy         807 GVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVER 866

Db         781 GVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVER 840

Qy         867 LISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRY 926

Db         841 LISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNRY 900

Qy         927 NILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIG 986

Db         901 NILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAYIG 960

Qy         987 GMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSA 1046

Db         961 GMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQFSA 1020

Qy        1047 MKMAHSPPGHHSVTGRPSV 1065

Db        1021 MKMAHSPPGHHSVTGRPSV 1039
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RESULT 14
US-09-849-602-26
; Sequence 26, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26

Query Match 96.0%; Score 5363.5; DB 3; Length 1227;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1035; Conservative 3; Mismatches 25; Indels 3; Gaps 2;

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Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065


RESULT 3
US-09-843-159B-3
; Sequence 3, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
;  APPLICANT: Luo, Yin
;  APPLICANT:  Chan, Evan
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Huang, Betty
;  TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
;  FILE REFERENCE: A-68292-2/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/843,159B
;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: US 09/696,668
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: US 09/427,154
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;  LENGTH: 1100
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-843-159B-3

  Query Match           100.0%;  Score 5585;  DB 2;  Length 1100;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1065;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60

Qy         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120

Qy        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180

Qy        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

Qy        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300

Qy        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360

Qy        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420

Qy        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

Qy        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540

Qy        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065


RESULT 4
US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT:  Gregg, Morin B.
;  APPLICANT:  Walter, Funk D.
;  APPLICANT:  Mieczyslaw, Piatyszek A.
;  TITLE OF INVENTION: A Second Mammalian Telomerase
;  FILE REFERENCE: 080/003C
;  CURRENT APPLICATION NUMBER: US/09/972,115A
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: US 60/128,577
;  PRIOR FILING DATE: 2000-04-10
;  PRIOR APPLICATION NUMBER: US 60/129,123
;  PRIOR FILING DATE: 1999-04-13
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;  LENGTH: 1166
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-972-115A-6

  Query Match           99.9%;  Score 5582;  DB 2;  Length 1166;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1064;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 126

Qy         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120
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Db        127 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 186

Qy        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180

Db        187 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 246

Qy        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

Db        247 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 306

Qy        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300

Db        307 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 366

Qy        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360

Db        367 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 426

Qy        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420

Db        427 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 486

Qy        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

Db        487 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546

Qy        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540

Db        547 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 606

Qy        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600

Db        607 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 666

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Db        667 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Db        727 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 786

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780

Db        787 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 846

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Db        847 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 906

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Db        907 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Db        967 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1026

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Db       1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1086

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065

Db       1087 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1131
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RESULT 5
US-09-696-668-4
; Sequence 4, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:

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;  APPLICANT: Luo, Ying
;  APPLICANT:  Chan, Eva
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Huang, Betty
;  APPLICANT:  Ossovskaya, Valeria
;  TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (
;  FILE REFERENCE: A-68292-1/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/696,668
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: US 09/427,154
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-696-668-4

  Query Match            99.9%;  Score 5582;  DB 2;  Length 1240;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1064;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60

Db        141 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 200

Qy         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120

Db        201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 260

Qy        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180

Db        261 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 320

Qy        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

Db        321 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380

Qy        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300

Db        381 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 440

Qy        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360

Db        441 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 500

Qy        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420

Db        501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 560

Qy        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

Db        561 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620

Qy        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540

Db        621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 680

Qy        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600

Db        681 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Db        741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Db        801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 860

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780
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Db        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIHYLLRGDAALLDAAKKGCLARVKKLSS 600

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Db        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Db        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780

Db        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Db        781 SFSELSSLVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Db        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Db        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Db        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065

Db       1021 -SCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1064


RESULT 9
US-09-350-982C-5
; Sequence 5, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
;  APPLICANT:  Berthelsen, Jens
;  APPLICANT:  Toma, Salvatore
;  APPLICANT:  Isacchi, Antonella
;  TITLE OF INVENTION:  Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Rela
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE:  PHRM-0043
;  CURRENT APPLICATION NUMBER: US/09/350,982C
;  CURRENT FILING DATE:  1999-07-09
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 5
;  LENGTH: 1166
;  TYPE: PRT
;  ORGANISM: Artificial
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Xaa is any amino acid
;  NAME/KEY: misc_feature
;  LOCATION: (1102)..(1102)
;  OTHER INFORMATION: n is any nucleic acid
;  NAME/KEY: misc_feature
;  LOCATION: (2650)..(2650)
;  OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-5

  Query Match             99.1%;  Score 5533;  DB 2;  Length 1166;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 1056;  Conservative    1;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GFGRKDVVEYLLQNGASVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 60

Db         67 GFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGADPNARDNWNYT 126

Qy         61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 120

Db        127 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTGEYKKDELLESAR 186

Qy        121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 180

Db        187 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADVHAKDKGDLV 246

Qy        181 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240

Db        247 PLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 306

Qy        241 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 300

Db        307 NCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHLSLEMVNFKHPQTHET 366

Qy        301 ALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVASEKAHNDVVEVVVKHEAKV 360

Db        367 AXHCAAASPYPKRKQICELLLRKGAXINEKTKEFLTPLHVASEKAHNDXVEVVVKHEAKV 426

Qy        361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 420

Db        427 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQGFTALQMGNENVQQLLQEGIS 486

Qy        421 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480

Db        487 LGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546

Qy        481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 540

Db        547 QHGADVHAKDKXXLVPLHNACSYGHYEVAELLVKHGAVVNVADLWKFTPLHEAAAKGKYE 606

Qy        541 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 600

Db        607 ICKLLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKSCLARVKKLSS 666

Qy        601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Db        667 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726

Qy        661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVS 720

Db        727 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTQLCALXLAHGADPTLKNQEGQTPLDLVS 786

Qy        721 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 780

Db        787 ADDVSALLTAAMPPSALPSCYKPQVLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSG 846

Qy        781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVE 840

Db        847 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSITQFVRXLGLEHLMDIFEREQITLDVLVE 906

Qy        841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900

Db        907 MGHKELKEIGINAYGHRHKLIKGVERLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966

Qy        901 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

Db        967 SVEEEMQSTVREHRDGGHAGGIFNRYNILKIQKVCNKKLWERYTHRRKEVSEENHNHANE 1026

Qy        961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1020

Db       1027 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKD 1086

Qy       1021 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1065

Db       1087 RSCYICHRQLLFCRVTLGKSFLQFSAMKMAHSPPGHHSVTGRPSV 1131


RESULT 10
US-09-849-602-26
; Sequence 26, Application US/09849602
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